

#13
KP
5-16-01

1632

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/321,987B

DATE: 05/01/2001
TIME: 17:53:32

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MAY 15 2001

TECH CENTER 1600/2900

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See p.5

3 <110> APPLICANT: Kimble, Judith E
4 Blelloch, Robert H
6 <120> TITLE OF INVENTION: Agent and Method for Modulating Cell Migration
8 <130> FILE REFERENCE: 960296.95386
10 <140> CURRENT APPLICATION NUMBER: 09/321,987B
11 <141> CURRENT FILING DATE: 1999-05-28
13 <150> PRIOR APPLICATION NUMBER: 60/087,170
14 <151> PRIOR FILING DATE: 1998-05-29
16 <150> PRIOR APPLICATION NUMBER: 60/129,023
17 <151> PRIOR FILING DATE: 1999-04-13
19 <160> NUMBER OF SEQ ID NOS: 5
21 <170> SOFTWARE: PatentIn Ver. 2.1
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24 <211> LENGTH: 6659
25 <212> TYPE: DNA
26 <213> ORGANISM: Caenorhabditis elegans
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30 <222> LOCATION: (1)..(6450) ✓
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35 1 5 10 15
37 gct ctc ata ctc ctc gtc gtc tgc ctc gtt tat gcg ttg caa tca ggg 96
38 Ala Leu Ile Leu Leu Val Val Cys Leu Val Tyr Ala Leu Gln Ser Gly
39 20 25 30
41 agt ggc acg atc tca gaa ttc tca tca gat gtg ctg ttc tcc agg gcc 144
42 Ser Gly Thr Ile Ser Glu Phe Ser Ser Asp Val Leu Phe Ser Arg Ala
43 35 40 45
45 aag tac tca ggt gtg cca gtg cat cac agt cga tgg cgt caa gac gcc 192
46 Lys Tyr Ser Gly Val Pro Val His His Ser Arg Trp Arg Gln Asp Ala
47 50 55 60
49 ggt ata cac gtc atc gac agc cat cac atc gtc cga aga gat tct tat 240
50 Gly Ile His Val Ile Asp Ser His His Ile Val Arg Arg Asp Ser Tyr
51 65 70 75 80
53 gga cgt cgt gga aaa cgt gat gtc acg tca aca gat cgg cga cgt cga 288
54 Gly Arg Arg Gly Lys Arg Asp Val Thr Ser Thr Asp Arg Arg Arg Arg
55 85 90 95
57 ctc caa gga gtt gcc aga gac tgt gga cat gct tgt cac tta cga tta 336
58 Leu Gln Gly Val Ala Arg Asp Cys Gly His Ala Cys His Leu Arg Leu
59 100 105 110
61 cga tca gat gat gcc gtc tac atc gtt cat ttg cac aga tgg aat caa 384
62 Arg Ser Asp Asp Ala Val Tyr Ile Val His Leu His Arg Trp Asn Gln
63 115 120 125
65 ata ccg gac tca cat aac aaa agt gtt ccc cac ttt tcc aat tca aat 432
66 Ile Pro Asp Ser His Asn Lys Ser Val Pro His Phe Ser Asn Ser Asn
67 130 135 140

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70 Phe Ala Pro Met Val Leu Tyr Leu Asp Ser Glu Glu Glu Val Arg Gly
71 145 150 155 160
73 gga atg tct cga aca gat ccc gat tgt atc tac cgt gca cac gtt aaa 528
74 Gly Met Ser Arg Thr Asp Pro Asp Cys Ile Tyr Arg Ala His Val Lys
75 165 170 175
77 ggt gta cat cag cac agc atc gtc aat tta tgc gac tcg gaa gac gga 576
78 Gly Val His Gln His Ser Ile Val Asn Leu Cys Asp Ser Glu Asp Gly
79 180 185 190
81 ttg tac gga atg ctt gca cta ccc agc gga atc cat acg gtt gag cca 624
82 Leu Tyr Gly Met Leu Ala Leu Pro Ser Gly Ile His Thr Val Glu Pro
83 195 200 205
85 att att agt gga aac gga aca gag cac gac gga gca agt cgc cat agg 672
86 Ile Ile Ser Gly Asn Gly Thr Glu His Asp Gly Ala Ser Arg His Arg
87 210 215 220
89 caa cat ctc gtc cga aag ttc gat cca atg cac ttc aaa tcg ttt gac 720
90 Gln His Leu Val Arg Lys Phe Asp Pro Met His Phe Lys Ser Phe Asp
91 225 230 235 240
93 cat ctt aac tcg acc agt gtc aac gag acg gag acg acg gtt gcc acg 768
94 His Leu Asn Ser Thr Ser Val Asn Glu Thr Glu Thr Thr Val Ala Thr
95 245 250 255
97 tgg caa gat cag tgg gaa gat gtt att gaa cgc aaa gca aga tcc cga 816
98 Trp Gln Asp Gln Trp Glu Asp Val Ile Glu Arg Lys Ala Arg Ser Arg
99 260 265 270
101 aga gct gcc aac tct tgg gat cac tat gtt gaa gtc ctt gtg gtg gcg 864
102 Arg Ala Ala Asn Ser Trp Asp His Tyr Val Glu Val Leu Val Val Ala
103 275 280 285
105 gat aca aaa atg tac gaa tat cac gga aga tct ctt gaa gac tac gtt 912
106 Asp Thr Lys Met Tyr Glu Tyr His Gly Arg Ser Leu Glu Asp Tyr Val
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109 ctc act ctc ttc tcc aca gtt gcc tcc atc tat cgt cac caa tcc ctt 960
110 Leu Thr Leu Phe Ser Thr Val Ala Ser Ile Tyr Arg His Gln Ser Leu
111 305 310 315 320
113 cgt gca tct atc aat gtc gtt gtt gtc aag ttg atc gtt ttg aaa acg 1008
114 Arg Ala Ser Ile Asn Val Val Val Val Lys Leu Ile Val Leu Lys Thr
115 325 330 335
117 gaa aac gct gga cca cga atc act cag aac gct caa caa aca ctt caa 1056
118 Glu Asn Ala Gly Pro Arg Ile Thr Gln Asn Ala Gln Gln Thr Leu Gln
119 340 345 350
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122 Asp Phe Cys Arg Trp Gln Gln Tyr Tyr Asn Asp Pro Asp Asp Ser Ser
123 355 360 365
125 gtc caa cat cat gac gtt gca atc ctt ttg acg cgt aaa gat att tgt 1152
126 Val Gln His His Asp Val Ala Ile Leu Leu Thr Arg Lys Asp Ile Cys
127 370 375 380
129 cga toa caa gga aaa tgc gat aca ctt gga ctt gct gaa ctt gga aca 1200
130 Arg Ser Gln Gly Lys Cys Asp Thr Leu Gly Leu Ala Glu Leu Gly Thr
131 385 390 395 400
133 atg tgt gat atg caa aaa agt tgt gca atc ata gaa gac aat gga ttg 1248

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137	agt	got	gca	ttc	aca	att	gct	cat	gaa	ttg	ggt	cat	gtg	ttt	tcg	att	1296
138	Ser	Ala	Ala	Phe	Thr	Ile	Ala	His	Glu	Leu	Gly	His	Val	Phe	Ser	Ile	
139				420					425					430			
141	cct	cat	gat	gac	gaa	cga	aaa	tgc	tct	acc	tac	atg	ccg	ggt	aat	aag	1344
142	Pro	His	Asp	Asp	Glu	Arg	Lys	Cys	Ser	Thr	Tyr	Met	Pro	Val	Asn	Lys	
143				435				440					445				
145	aac	aac	ttc	cac	ata	atg	gca	cca	acg	ttg	gaa	tat	aac	act	cat	cca	1392
146	Asn	Asn	Phe	His	Ile	Met	Ala	Pro	Thr	Leu	Glu	Tyr	Asn	Thr	His	Pro	
147				450			455					460					
149	tgg	agt	tgg	tcg	cca	tgt	tca	gct	gga	atg	ctc	gaa	cga	ttc	ctc	gaa	1440
150	Trp	Ser	Trp	Ser	Pro	Cys	Ser	Ala	Gly	Met	Leu	Glu	Arg	Phe	Leu	Glu	
151	465				470					475					480		
153	aat	aat	cga	ggt	caa	act	caa	tgt	cta	ttc	gat	cag	ccg	gtc	gaa	cgt	1488
154	Asn	Asn	Arg	Gly	Gln	Thr	Gln	Cys	Leu	Phe	Asp	Gln	Pro	Val	Glu	Arg	
155				485					490					495			
157	cgt	tac	tac	gag	gat	gtc	ttt	gta	cgt	gat	gaa	cca	gga	aag	aaa	tac	1536
158	Arg	Tyr	Tyr	Glu	Asp	Val	Phe	Val	Arg	Asp	Glu	Pro	Gly	Lys	Lys	Tyr	
159				500				505					510				
161	gat	gct	cat	caa	cag	tgc	aag	ttt	gta	ttt	gga	cca	gct	tct	gag	ttg	1584
162	Asp	Ala	His	Gln	Gln	Cys	Lys	Phe	Val	Phe	Gly	Pro	Ala	Ser	Glu	Leu	
163				515				520				525					
165	tgc	cct	tat	atg	ccg	aca	tgc	cgc	cgt	ctt	tgg	tgt	gca	aca	ttc	tac	1632
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171	545				550				555						560		
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174	Thr	Pro	Cys	Asp	Glu	Ser	Arg	Ser	Met	Phe	Cys	His	His	Gly	Ala	Cys	
175				565				570					575				
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178	Val	Arg	Leu	Ala	Pro	Glu	Ser	Leu	Thr	Lys	Ile	Asp	Gly	Gln	Trp	Gly	
179				580				585					590				
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182	Asp	Trp	Arg	Ser	Trp	Gly	Glu	Cys	Ser	Arg	Thr	Cys	Gly	Gly	Gly	Val	
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186	Gln	Lys	Gly	Leu	Arg	Asp	Cys	Asp	Ser	Pro	Lys	Pro	Arg	Asn	Gly	Gly	
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190	Lys	Tyr	Cys	Val	Gly	Gln	Arg	Glu	Arg	Tyr	Arg	Ser	Cys	Asn	Thr	Gln	
191	625				630				635						640		
193	gaa	tgc	cca	tgg	gat	act	caa	cca	tac	cgt	gaa	gtt	caa	tgt	tct	gaa	1968
194	Glu	Cys	Pro	Trp	Asp	Thr	Gln	Pro	Tyr	Arg	Glu	Val	Gln	Cys	Ser	Glu	
195				645				650					655				
197	ttc	aac	aat	aaa	gat	att	gga	atc	caa	ggt	gtc	gct	tca	acg	aat	act	2016
198	Phe	Asn	Asn	Lys	Asp	Ile	Gly	Ile	Gln	Gly	Val	Ala	Ser	Thr	Asn	Thr	

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203		675		680		685		
205	ctg tat tgt	cgg ctc agt	gga tct gca	gcg ttc tat	ctg ctt cga	gat	2112	
206	Leu Tyr Cys	Arg Leu Ser	Gly Ser Ala	Ala Phe Tyr	Leu Leu Arg	Asp		
207		690		695		700		
209	aaa gtt gtt	gat gga aca	cca tgt gat	aga aat gga	gac gat att	tgt	2160	
210	Lys Val Val	Asp Gly Thr	Pro Cys Asp	Arg Asn Gly	Asp Asp Ile	Cys		
211	705		710		715	720		
213	gta gct gga	gct tgt atg	cca gca ggc	tgt gat cat	caa ctt cat	tca	2208	
214	Val Ala Gly	Ala Cys Met	Pro Ala Gly	Cys Asp His	Gln Leu His	Ser		
215		725		730		735		
217	act ctc cga	aga gac aaa	tgt ggt gtt	tgc ggt ggg	gat gat tct	tcc	2256	
218	Thr Leu Arg	Arg Asp Lys	Cys Gly Val	Cys Gly Gly	Asp Asp Ser	Ser		
219		740		745		750		
221	tgt aag gtt	gtc aaa gga	aca ttt aat	gag caa gga	acc ttt ggt	tat	2304	
222	Cys Lys Val	Val Lys Gly	Thr Phe Asn	Glu Gln Gly	Thr Phe Gly	Tyr		
223		755		760		765		
225	aac gaa gta	atg aag att	cca gct ggt	tct gca aat	att gat atc	cgg	2352	
226	Asn Glu Val	Met Lys Ile	Pro Ala Gly	Ser Ala Asn	Ile Asp Ile	Arg		
227		770		775		780		
229	cag aaa gga	tat aat aat	atg aaa gaa	gat gac aat	tat ctt tct	ctc	2400	
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231	785		790		795	800		
233	cgt gcc gcc	aat ggt gaa	ttc cta ctt	aac ggt cat	ttc caa gta	tca	2448	
234	Arg Ala Ala	Asn Gly Glu	Phe Leu Leu	Asn Gly His	Phe Gln Val	Ser		
235		805		810		815		
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238	Leu Ala Arg	Gln Gln Ile	Ala Phe Gln	Asp Thr Val	Leu Glu Tyr	Ser		
239		820		825		830		
241	ggt tct gat	gca att att	gaa cgg ata	aat gga act	ggt ccg att	aga	2544	
242	Gly Ser Asp	Ala Ile Ile	Glu Arg Ile	Asn Gly Thr	Gly Pro Ile	Arg		
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254	Pro Ile Ser	Ser Ala Leu	Tyr Leu Trp	Arg Val Thr	Asp Thr Trp	Thr		
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261	ctg gac atg	tcg act cat	cgt caa agt	cat gat aga	aat tgt caa	aat	2784	
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VERIFICATION SUMMARY

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Output Set: N:\CRF3\05012001\I321987B.raw

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1	CTFR	9

Total number of pages: 9

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